

Patent Application US/07/952,640

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: CROWE, JAMES SCOTT  
LEWIS, ALAN PETER

(ii) TITLE OF INVENTION: PRODUCTION OF ANTIBODIES

(iii) NUMBER OF SEQUENCES: 46

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ  
(B) STREET: 555 THIRTEENTH ST. N.W.  
(C) CITY: WASHINGTON  
(D) STATE: D. C.  
(E) COUNTRY: U.S.  
(F) ZIP: 20004

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/952640  
(B) FILING DATE: 01-DEC-1992  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: ERNST, BARBARA G  
(B) REGISTRATION NUMBER: 30,377  
(C) REFERENCE/DOCKET NUMBER: 1808-118

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202) 783-6040  
(B) TELEFAX: (202) 783-6031

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Au 1806

#8

-see p. 11, 4

32 → 37

## Patent Application US/07/952,640

53  
54 GACATTCAGC TGACCCAGTC TCCA 24  
55  
56 (2) INFORMATION FOR SEQ ID NO:2:  
57  
58 (i) SEQUENCE CHARACTERISTICS:  
59 (A) LENGTH: 24 base pairs  
60 (B) TYPE: nucleic acid  
61 (C) STRANDEDNESS: single  
62 (D) TOPOLOGY: linear  
63  
64 (ii) MOLECULE TYPE: DNA (genomic)  
65  
66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
67  
68 GATCAAGCTT CTAACACTCT CCCC 24  
69  
70 (2) INFORMATION FOR SEQ ID NO:3:  
71  
72 (i) SEQUENCE CHARACTERISTICS:  
73 (A) LENGTH: 34 base pairs  
74 (B) TYPE: nucleic acid  
75 (C) STRANDEDNESS: single  
76 (D) TOPOLOGY: linear  
77  
78 (ii) MOLECULE TYPE: DNA (genomic)  
79  
80 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
81  
82 GATCAAGCTT GACATTCAGC TGACCCAGTC TCCA 34  
83  
84 (2) INFORMATION FOR SEQ ID NO:4:  
85  
86 (i) SEQUENCE CHARACTERISTICS:  
87 (A) LENGTH: 16 base pairs  
88 (B) TYPE: nucleic acid  
89 (C) STRANDEDNESS: single  
90 (D) TOPOLOGY: linear  
91  
92 (ii) MOLECULE TYPE: DNA (genomic)  
93  
94 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
95  
96 AACAGCTATG ACCATG 16  
97  
98 (2) INFORMATION FOR SEQ ID NO:5:  
99  
100 (i) SEQUENCE CHARACTERISTICS:  
101 (A) LENGTH: 17 base pairs  
102 (B) TYPE: nucleic acid  
103 (C) STRANDEDNESS: single  
104 (D) TOPOLOGY: linear

## Patent Application US/07/952,640

105  
106 (ii) MOLECULE TYPE: DNA (genomic)  
107  
108 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
109  
110 GTTTTCCCAG TCACGAC 17  
111  
112 (2) INFORMATION FOR SEQ ID NO:6:  
113  
114 (i) SEQUENCE CHARACTERISTICS:  
115 (A) LENGTH: 20 base pairs  
116 (B) TYPE: nucleic acid  
117 (C) STRANDEDNESS: single  
118 (D) TOPOLOGY: linear  
119  
120 (ii) MOLECULE TYPE: DNA (genomic)  
121  
122 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
123  
124 GCGTCAGGGT GCTGCTGAGG 20  
125  
126 (2) INFORMATION FOR SEQ ID NO:7:  
127  
128 (i) SEQUENCE CHARACTERISTICS:  
129 (A) LENGTH: 20 base pairs  
130 (B) TYPE: nucleic acid  
131 (C) STRANDEDNESS: single  
132 (D) TOPOLOGY: linear  
133  
134 (ii) MOLECULE TYPE: DNA (genomic)  
135  
136 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:  
137  
138 GGCGGGAAGA TGAAGACAGA 20  
139  
140 (2) INFORMATION FOR SEQ ID NO:8:  
141  
142 (i) SEQUENCE CHARACTERISTICS:  
143 (A) LENGTH: 20 base pairs  
144 (B) TYPE: nucleic acid  
145 (C) STRANDEDNESS: single  
146 (D) TOPOLOGY: linear  
147  
148 (ii) MOLECULE TYPE: DNA (genomic)  
149  
150  
151  
152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:  
153  
154 TTCAGCAGGC ACACAACAGA 20  
155  
156 (2) INFORMATION FOR SEQ ID NO:9:

## Patent Application US/07/952,640

157  
158 (i) SEQUENCE CHARACTERISTICS:  
159 (A) LENGTH: 1617 base pairs  
160 (B) TYPE: nucleic acid  
161 (C) STRANDEDNESS: both  
162 (D) TOPOLOGY: linear  
163  
164 (ii) MOLECULE TYPE: cDNA  
165  
166 (iii) HYPOTHETICAL: NO  
167  
168 (iv) ANTI-SENSE: NO  
169  
170  
171 (ix) FEATURE:  
172 (A) NAME/KEY: sig\_peptide  
173 (B) LOCATION: 35..92  
174  
175 (ix) FEATURE:  
176 (A) NAME/KEY: mat\_peptide  
177 (B) LOCATION: 93..1465  
178  
179 (ix) FEATURE:  
180 (A) NAME/KEY: CDS  
181 (B) LOCATION: 35..1465  
182  
183  
184 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:  
185  
186 TCTAAAGAAG CCCCTGGGAG CACAGCTCAT CACC ATG GAC TGG ACC TGG AGG 52  
187 Met Asp Trp Thr Trp Arg  
188 -19 -15  
189  
190 TTC CTC TTT GTG GTG GCA GCA GCT ACA GGT GTC CAG TCC CAG ATG CAG 100  
191 Phe Leu Phe Val Val Ala Ala Ala Thr Gly Val Gln Ser Gln Met Gln  
192 -10 -5 1  
193  
194 GTG GTG CAG TCT GGG GCT GAA GTA AAG AAG CCT GGG TCC TCG GTG ACG 148  
195 Val Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Thr  
196 5 10 15  
197  
198 GTC TCC TGC AAG GCA TCT GGA GGC ACC TTC AGC AAC TAT GCT ATC AGC 196  
199 Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asn Tyr Ala Ile Ser  
200 20 25 30 35  
201  
202 TGG GTG CGA CAG GCC CCT GGA CAA GGG CTT GAG TGG ATG GGA GGG ATC 244  
203 Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile  
204 40 45 50  
205  
206 ATC CCT CTT TTT GGT ACA CCA ACC TAC TCA CAG AAC TTC CAG GGC AGA 292  
207 Ile Pro Leu Phe Gly Thr Pro Thr Tyr Ser Gln Asn Phe Gln Gly Arg  
208 55 60 65

## Patent Application US/07/952,640

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209
210 GTC ACG ATT ACC GCG GAC AAA TCC ACC AGC ACA GCC CAC ATG GAG CTG      340
211 Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala His Met Glu Leu
212      70      75      80
213
214 ACT AGC CTG AGA TCT GAG GAC ACG GCC GTG TAT TAC TGT GCG ACA GAT      388
215 Thr Ser Leu Arg Ser Glu Aep Thr Ala Val Tyr Tyr Cys Ala Thr Asp
216      85      90      95
217
218 CGC TAC AGG CAG GCA AAT TTT GAC CGG GCC CGG GTT GGC TGG TTC GAC      436
219 Arg Tyr Arg Gln Ala Asn Phe Asp Arg Ala Arg Val Gly Trp Phe Aep
220 100      105      110      115
221
222 CCC TGG GGC CAG GGC ACC CTG GTC ACC GTC TCC TCA GCC TCC ACC AAG      484
223 Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
224      120      125      130
225
226 GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG      532
227 Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
228      135      140      145
229
230 GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG      580
231 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Aep Tyr Phe Pro Glu Pro
232      150      155      160
233
234 GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC GTG CAC ACC      628
235 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
236      165      170      175
237
238 TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG      676
239 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
240 180      185      190      195
241
242 GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC TAC ATC TGC AAC      724
243 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
244      200      205      210
245
246 GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG CCC      772
247 Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
248      215      220      225
249
250 AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA      820
251 Lys Ser Cys Aep Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
252      230      235      240
253
254 CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC      868
255 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
256      245      250      255
257
258 ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC      916
259 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Aep
260 260      265      270      275

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## Patent Application US/07/952,640

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261
262   GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC           964
263   Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
264               280               285               290
265
266   GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC           1012
267   Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
268               295               300               305
269
270   AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG           1060
271   Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
272               310               315               320
273
274   CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA           1108
275   Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
276               325               330               335
277
278   GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA           1156
279   Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
280   340               345               350               355
281
282   CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC           1204
283   Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
284               360               365               370
285
286   CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC           1252
287   Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
288               375               380               385
289
290   GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC           1300
291   Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
292               390               395               400
293
294   ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG           1348
295   Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
296               405               410               415
297
298   CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC           1396
299   Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
300   420               425               430               435
301
302   TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC           1444
303   Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
304               440               445               450
305
306   TCC CTG TCT CCG GGT AAA TGAGTGCAGAC GGCCGGCAAG CCCCCGCTCC           1492
307   Ser Leu Ser Pro Gly Lys
308               455
309
310   CCGGGCTCTC GCGGTCGCAC GAGGATGCTT GGCACGTACC CCGTGTACAT ACTTCCCGGG           1552
311
312   CGCCCAGCAT GGAAATAAAG CACCCAGCGC TGCCCTGGGC CCCTGCGAAA AAAAAAAAAA           1612

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## Patent Application US/07/952,640

313  
314 AAAAA 1617  
315 (2) INFORMATION FOR SEQ ID NO:10:  
316  
317 (i) SEQUENCE CHARACTERISTICS:  
318 (A) LENGTH: 476 amino acids  
319 (B) TYPE: amino acid  
320 (D) TOPOLOGY: linear  
321  
322 (ii) MOLECULE TYPE: protein  
323  
324 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:  
325  
326 Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly  
327 -19 -15 -10 -5  
328  
329 Val Gln Ser Gln Met Gln Val Val Gln Ser Gly Ala Glu Val Lys Lys  
330 1 5 10  
331  
332 Pro Gly Ser Ser Val Thr Val Ser Cys Lys Ala Ser Gly Gly Thr Phe  
333 15 20 25  
334  
335 Ser Asn Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
336 30 35 40 45  
337  
338 Glu Trp Met Gly Gly Ile Ile Pro Leu Phe Gly Thr Pro Thr Tyr Ser  
339 50 55 60  
340  
341 Gln Asn Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser  
342 65 70 75  
343  
344 Thr Ala His Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val  
345 80 85 90  
346  
347 Tyr Tyr Cys Ala Thr Asp Arg Tyr Arg Gln Ala Asn Phe Asp Arg Ala  
348 95 100 105  
349  
350 Arg Val Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val  
351 110 115 120 125  
352  
353 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
354 130 135 140  
355  
356 Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
357 145 150 155  
358  
359 Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
360 160 165 170  
361  
362 Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
363 175 180 185  
364

**Patent Application US/07/952,640**

365	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr
366	190					195				200					205	
367																
368	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val
369					210					215					220	
370																
371	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro
372				225					230					235		
373																
374	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
375			240					245					250			
376																
377	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
378		255					260					265				
379																
380	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe
381	270					275					280					285
382																
383	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
384				290						295					300	
385																
386	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
387				305					310					315		
388																
389	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
390			320					325					330			
391																
392	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
393		335					340					345				
394																
395	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg
396	350					355					360					365
397																
398	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
399					370					375					380	
400																
401	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
402				385					390					395		
403																
404	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
405			400					405					410			
406																
407	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln
408		415					420					425				
409																



## Patent Application US/07/952,640

417 (2) INFORMATION FOR SEQ ID NO:11:

418

419 (i) SEQUENCE CHARACTERISTICS:

420 (A) LENGTH: 902 bass pairs

421 (B) TYPE: nuclsic acid

422 (C) STRANDEDNESS: both

423 (D) TOPOLOGY: linear

424

425 (ii) MOLECULE TYPE: cDNA

426

427 (iii) HYPOTHETICAL: NO

428

429 (iv) ANTI-SENSE: NO

430

431

432 (ix) FEATURE:

433 (A) NAME/KEY: CDS

434 (B) LOCATION: 32..739

435

436 (ix) FEATURE:

437 (A) NAME/KEY: mat\_psptids

438 (B) LOCATION: 89..739

439

440 (ix) FEATURE:

441 (A) NAME/KEY: sig\_peptide

442 (B) LOCATION: 32..86

443

444

445 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

446

447 CAAGAGGCAG CGCTCTCGGG ACGTCTCCAC C ATG GCC TGG GCT CTG CTG CTC 52

448 Mst Ala Trp Ala Lsu Lsu Lsu

449 -19 -15

450

451 CTC ACC CTC CTC ACT CAG GAC ACA GGG TCC TGG GCC CAG TCT GCC CTG 100

452 Leu Thr Leu Leu Thr Gln Asp Thr Gly Ser Trp Ala Gln Ssr Ala Lsu

453 -10 -5 1

454

455 ACT CAG CCT GCC TCC GTG TCT GGG TCT CCT GGA CAG TCG ATC ACC ATC 148

456 Thr Gln Pro Ala Ser Val Ser Gly Ssr Pro Gly Gln Ssr Ils Thr Ils

457 5 10 15 20

458

459 TCC TGC ACT GGA ACC AAC AAT GAT GTT GGG AGT TAT AAC CTT GTC TCC 196

460 Ser Cys Thr Gly Thr Asn Asn Asp Val Gly Ssr Tyr Asn Lsu Val Ser

461 25 30 35

462

463 TGG TAC CAG CAG CAC CCA GGC AAA GCC CCC AAA ATC ATG ATT TAT GAG 244

464 Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Ils Met Ile Tyr Glu

465 40 45 50

466

467 GTC AGT AAG CGG CCC TCA GGG GTT TCT AAT CGC TTC TCT GGC TCC AAG 292

468 Val Ser Lys Arg Pro Ser Gly Val Ssr Asn Arg Phs Ser Gly Ssr Lys

## Patent Application US/07/952,640

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469          55          60          65
470
471 TCT GGC AAC ACG GCC TCC CTG ACA ATC TCT GGG CTC CAG GCT GAG GAC      340
472 Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp
473      70      75      80
474
475 GAG GCT GAT TAT TAC TGC TGC TCA TAT GCA GGT AGT TAC ACT GTG GTT      388
476 Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr Ala Gly Ser Tyr Thr Val Val
477      85      90      95      100
478
479 TTC GGC GGA GGG ACC AAA CTG ACC GTC CTA GGT CAG CCC AAG GCT GCC      436
480 Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala
481      105      110      115
482
483 CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT GAG GAG CTT CAA GCC AAC      484
484 Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
485      120      125      130
486
487 AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC TTC TAC CCG GGA GCC GTG      532
488 Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
489      135      140      145
490
491 ACA GTG GCC TGG AAG GCA GAT AGC AGC CCC GTC AAG GCG GGA GTG GAG      580
492 Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu
493      150      155      160
494
495 ACC ACC ACA CCC TCC AAA CAA AGC AAC AAC AAG TAC GCG GCC AGC AGC      628
496 Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser
497      165      170      175      180
498
499 TAT CTG AGC CTG ACG CCT GAG CAG TGG AAG TCC CAC AGA AGC TAC AGC      676
500 Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser
501      185      190      195
502
503 TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG GAG AAG ACA GTG GCC CCT      724
504 Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro
505      200      205      210
506
507 ACA GAA TGT TCA TAGGTTCTAA ACCCTCACCC CCCCCACGGG AGACTAGAGC      776
508 Thr Glu Cys Ser
509      215
510
511 TGCAGGATCC CAGGGGAGGG GTCTCTCCTC CCACCCCAAG GCATCAAGCC CTTCTCCCTG      836
512
513 CACTCAATAA ACCCTCAATA AATATTCTCA TTGTCAATCA CAAAAAAAAA AAAAAAAAAA      896
514
515 AAAAAA      902
516
517
518 (2) INFORMATION FOR SEQ ID NO:12:
519
520 (i) SEQUENCE CHARACTERISTICS:
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## Patent Application US/07/952,640

521 (A) LENGTH: 235 amino acids  
522 (B) TYPE: amino acid  
523 (D) TOPOLOGY: linear  
524  
525 (ii) MOLECULE TYPE: protein  
526  
527 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:  
528  
529 Met Ala Trp Ala Leu Leu Leu Thr Leu Leu Thr Gln Asp Thr Gly  
530 -19 -15 -10 -5  
531  
532 Ser Trp Ala Gln Ser Als Leu Thr Gln Pro Ala Ser Val Ser Gly Ser  
533 1 5 10  
534  
535 Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Aen Asn Asp Val  
536 15 20 25  
537  
538 Gly Ser Tyr Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala  
539 30 35 40 45  
540  
541 Pro Lye Ile Met Ile Tyr Glu Val Ser Lye Arg Pro Ser Gly Val Ser  
542 50 55 60  
543  
544 Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile  
545 65 70 75  
546  
547 Ser Gly Leu Gln Ala Glu Aep Glu Ala Aep Tyr Tyr Cye Cys Ser Tyr  
548 80 85 90  
549  
550 Ala Gly Ser Tyr Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val  
551 95 100 105  
552  
553 Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser  
554 110 115 120 125  
555  
556 Ser Glu Glu Leu Gln Ala Aen Lys Als Thr Leu Val Cys Leu Ile Ser  
557 130 135 140  
558  
559 Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Aep Ser Ser  
560 145 150 155  
561  
562 Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn  
563 160 165 170  
564  
565 Aen Lye Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp  
566 175 180 185  
567  
568 Lye Ser Hie Arg Ser Tyr Ser Cys Gln Val Thr Hie Glu Gly Ser Thr  
569 190 195 200 205  
570  
571 Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  
572 210 215

(2) INFORMATION FOR SEQ ID NO:13:

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page break" code,  
if present).

## Patent Application US/07/952,640

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573
574      (i) SEQUENCE CHARACTERISTICS:
575          (A) LENGTH: 321 base pairs
576          (B) TYPE: nucleic acid
577          (C) STRANDEDNESS: both
578          (D) TOPOLOGY: linear
579
580      (ii) MOLECULE TYPE: cDNA
581
582      (iii) HYPOTHETICAL: NO
583
584      (iv) ANTI-SENSE: NO
585
586
587      (ix) FEATURE:
588          (A) NAME/KEY: CDS
589          (B) LOCATION: 1..321
590
591
592      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
593
594      GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA      48
595      Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
596      1          5          10          15
597
598      GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AAT TAT      96
599      Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
600      20          25          30
601
602      TTA AAT TGG TAT CAA CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC      144
603      Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
604      35          40          45
605
606      TAT GCT GCA TCC AGT TTG CAA AGT GGG GTC ACA TCA AGG TTC AGT GGC      192
607      Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Thr Ser Arg Phe Ser Gly
608      50          55          60
609
610      AGT GGA TCT GGG ACA GAC TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT      240
611      Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
612      65          70          75          80
613
614      GAA GAT TCT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CTG ATC      288
615      Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Ile
616      85          90          95
617
618      ACC TTC GGC CAA GGG ACA CGA CTG GAG ATT AAA      321
619      Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
620      100          105
621
622
623      (2) INFORMATION FOR SEQ ID NO:14:
624

```

## Patent Application US/07/952,640

625 (i) SEQUENCE CHARACTERISTICS:  
626 (A) LENGTH: 107 amino acids  
627 (B) TYPE: amino acid  
628 (D) TOPOLOGY: linear  
629  
630 (ii) MOLECULE TYPE: protein  
631  
632 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:  
633  
634 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ssr Ala Ser Val Gly  
635 1 5 10 15  
636  
637 Asp Arg Val Thr Ile Thr Cys Arg Ala Ssr Gln Ssr Ile Ssr Asn Tyr  
638 20 25 30  
639  
640 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
641 35 40 45  
642  
643 Tyr Ala Ala Ssr Ser Leu Gln Ser Gly Val Thr Ssr Arg Phe Ssr Gly  
644 50 55 60  
645  
646 Ssr Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
647 65 70 75 80  
648  
649 Glu Asp Ssr Ala Thr Tyr Tyr Cys Gln Gln Ssr Tyr Ssr Thr Leu Ile  
650 85 90 95  
651  
652 Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
653 100 105  
654  
655 (2) INFORMATION FOR SEQ ID NO:15:  
656  
657 (i) SEQUENCE CHARACTERISTICS:  
658 (A) LENGTH: 324 base pairs  
659 (B) TYPE: nucleic acid  
660 (C) STRANDEDNESS: both  
661 (D) TOPOLOGY: linear  
662  
663 (ii) MOLECULE TYPE: cDNA  
664  
665 (iii) HYPOTHETICAL: NO  
666  
667 (iv) ANTI-SENSE: NO  
668  
669  
670 (ix) FEATURE:  
671 (A) NAME/KEY: CDS  
672 (B) LOCATION: 1..324  
673  
674  
675 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:  
676

## Patent Application US/07/952,640

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677 GAC ATT CAG CTG ACC CAG TCT CCA TCT TCC CTG TCT GCA TCG GTA GGA      48
678 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
679   1               5               10               15
680
681 GAC AGA GTC ACC ATC ACC TGC AGG GCA AGT CAG GGC ATT AGC GAT TAT      96
682 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
683   20               25               30
684
685 TTA AGT TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT GAG CTC CTG ATC      144
686 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile
687   35               40               45
688
689 TAT GCT GCT TCC AGT TTG CAA AGT GGG ATT CCC TCT CGG TTC AGC GGC      192
690 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
691   50               55               60
692
693 AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT      240
694 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
695   65               70               75               80
696
697 GAA GAT TCT GCA GTT TAT TAC TGT CAA CAC ACT TAT AGT GAC CCG TAC      288
698 Glu Asp Ser Ala Val Tyr Tyr Cys Gln His Thr Tyr Ser Asp Pro Tyr
699   85               90               95
700
701 AGT TTT GGC CAG GGG ACC AAA GTG GAC ATC AAA CGA      324
702 Ser Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg
703   100               105
704
705
706 (2) INFORMATION FOR SEQ ID NO:16:
707
708 (i) SEQUENCE CHARACTERISTICS:
709 (A) LENGTH: 108 amino acids
710 (B) TYPE: amino acid
711 (D) TOPOLOGY: linear
712
713 (ii) MOLECULE TYPE: protein
714
715 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
716
717 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
718   1               5               10               15
719
720 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
721   20               25               30
722
723 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile
724   35               40               45
725
726 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
727   50               55               60
728
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## Patent Application US/07/952,640

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729 Ser Gly Ser Gly Thr Aep Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
730 65                      70                      75                      80
731
732 Glu Aep Ser Ala Val Tyr Tyr Cye Gln Hie Thr Tyr Ser Aep Pro Tyr
733                      85                      90                      95
734
735 Ser Phe Gly Gln Gly Thr Lye Val Asp Ile Lys Arg
736          100                      105
737

```

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..324

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

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759
760 GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCT TCT GTA GGA      48
761 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
762 1                      5                      10                      15
763
764 GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG GGC ATT AGC ACT TAT      96
765 Aep Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Tyr
766          20                      25                      30
767
768 TTA AGT TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC      144
769 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
770          35                      40                      45
771
772 TAT TAT GCA AAC AGT TTG GCA AGT GGG GTC CCA TCA AGG TTC AGC GGC      192
773 Tyr Tyr Ala Asn Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
774          50                      55                      60
775
776 AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT      240
777 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
778 65                      70                      75                      80
779
780 GAA GAT TCT GCA ACT TAT TAC TGT GGA CAG GGT AAT AGT TAC CCT CTC      288

```

## Patent Application US/07/952,640

781 Glu Asp Ser Ala Thr Tyr Tyr Cys Gly Gln Gly Asn Ser Tyr Pro Leu  
782 85 90 95

783  
784 ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA 324  
785 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
786 100 105

787  
788  
789 (2) INFORMATION FOR SEQ ID NO:18:

790  
791 (i) SEQUENCE CHARACTERISTICS:  
792 (A) LENGTH: 108 amino acids  
793 (B) TYPE: amino acid  
794 (D) TOPOLOGY: linear

795  
796 (ii) MOLECULE TYPE: protein

797  
798 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

799  
800 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
801 1 5 10 15

802  
803 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Tyr  
804 20 25 30

805  
806 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
807 35 40 45

808  
809 Tyr Tyr Ala Asn Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly  
810 50 55 60

811  
812 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
813 65 70 75 80

814  
815 Glu Asp Ser Ala Thr Tyr Tyr Cys Gly Gln Gly Asn Ser Tyr Pro Leu  
816 85 90 95

817  
818 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
819 100 105

820  
821 (2) INFORMATION FOR SEQ ID NO:19:

822  
823 (i) SEQUENCE CHARACTERISTICS:  
824 (A) LENGTH: 324 base pairs  
825 (B) TYPE: nucleic acid  
826 (C) STRANDEDNESS: both  
827 (D) TOPOLOGY: linear

828  
829 (ii) MOLECULE TYPE: cDNA

830  
831 (iii) HYPOTHETICAL: NO

832



## Patent Application US/07/952,640

833 (iv) ANTI-SENSE: NO

834

835

836 (ix) FEATURE:

837 (A) NAME/KEY: CDS

838 (B) LOCATION: 1..324

839

840

841 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

842

843 GAC ATT CAG CTG ACC CAG TCT CCA TCC TCT CAG TCT GCA TCT GTA GGA 48

844 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Gln Ser Ala Ser Val Gly

845 1 5 10 15

846

847 GAC AGA GTG ACC ATT ACT TGC CAG GCG AGT CAA AGC CTT AGC AAT TAT 96

848 Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Leu Ser Asn Tyr

849 20 25 30

850

851 TTA AAT TGG TAT CAG CAG AAA CCA GGG AAA ATT CCT AAG CTC CTG ATC 144

852 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile

853 35 40 45

854

855 TAT AGG GCA TCC AGT TTG CAA AGT GGG ATT CCC TCT CGG TTC AGC GGC 192

856 Tyr Arg Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly

857 50 55 60

858

859 AGT GGA TCT GGG ACG GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT 240

860 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

861 65 70 75 80

862

863 GAA GAT TTT GCC ACT TAT TAC TGT CAG CAT AAT TAT GGT ACC CCT CTC 288

864 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asn Tyr Gly Thr Pro Leu

865 85 90 95

866

867 ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA 324

868 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg

869 100 105

870

871

872 (2) INFORMATION FOR SEQ ID NO:20:

873

874 (i) SEQUENCE CHARACTERISTICS:

875 (A) LENGTH: 108 amino acids

876 (B) TYPE: amino acid

877 (D) TOPOLOGY: linear

878

879 (ii) MOLECULE TYPE: protein

880

881 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

882

883 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Gln Ser Ala Ser Val Gly

884 1 5 10 15

## Patent Application US/07/952,640

885  
886 Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Leu Ser Asn Tyr  
887 20 25 30  
888  
889 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Lsu Lsu Ile  
890 35 40 45  
891  
892 Tyr Arg Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly  
893 50 55 60  
894  
895 Ser Gly Ser Gly Thr Asp Phe Thr Lsu Thr Ile Ser Ser Lsu Gln Pro  
896 65 70 75 80  
897  
898 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asn Tyr Gly Thr Pro Lsu  
899 85 90 95  
900  
901 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
902 100 105  
903

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..324

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

921 GACATTCAGC TGACCCAGTC TCCACTCTCC CTGCCCCTCA GTCTTGGAGA GTCGGCCTCC 60  
922  
923 ATCTCCTNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 120  
924  
925 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNTCCCAGAC 180  
926  
927 AGGTTCAC TG CAGTGGGTC AGGCACTGAT TTCACACTGA AAATCAGCAG AGTGGAGGCT 240  
928  
929 GAGGATGTTG GGGTTTATTA CTGCATGCAA GCTCTTCGGT CTCCTTGGAC GTTCGGCCAA 300  
930  
931 GGGACCAAGG TGGAAATCAG ACGA 324  
932

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

## Patent Application US/07/952,640

937 (A) LENGTH: 108 amino acids  
938 (B) TYPE: amino acid  
939 (D) TOPOLOGY: linear  
940  
941 (ii) MOLECULE TYPE: protein  
942  
943 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:  
944  
945 Aep Ile Gln Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly  
946 1 5 10 15  
947  
948 Glu Ser Ala Ser Ile Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
949 20 25 30  
950  
951 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
952 35 40 45  
953  
954 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Asp Xaa Xaa Thr Xaa  
955 50 55 60  
956  
957 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Arg Val Glu Ala  
958 65 70 75 80  
959  
960 Xaa Xaa Val Gly Val Xaa Xaa Xaa Met Xaa Ala Leu Arg Ser Pro Trp  
961 85 90 95  
962  
963 Xaa Xaa Xaa Xaa Xaa Xaa Lye Val Xaa Xaa Arg Arg  
964 100 105  
965  
966  
967 (2) INFORMATION FOR SEQ ID NO:23:  
968  
969 (i) SEQUENCE CHARACTERISTICS:  
970 (A) LENGTH: 324 base pairs  
971 (B) TYPE: nucleic acid  
972 (C) STRANDEDNESS: both  
973 (D) TOPOLOGY: linear  
974  
975 (ii) MOLECULE TYPE: cDNA  
976  
977 (iii) HYPOTHETICAL: NO  
978  
979 (iv) ANTI-SENSE: NO  
980  
981  
982 (ix) FEATURE:  
983 (A) NAME/KEY: CDS  
984 (B) LOCATION: 1..324  
985  
986  
987 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:  
988

## Patent Application US/07/952,640

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989  GAC ATT CAG CTG ACC CAG TCT CCA TCT TCC CTG TCT GCA TCG GTA GGA      48
990  Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
991    1              5              10              15
992
993  GAC AGA GTC ACC ATC ACC TGC AGG GCA AGT CAG GGC ATT AGC GAT TAT      96
994  Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
995    20              25              30
996
997  TTA AGT TGG TAT CAG CAG AAA CCA GGA AAA GCT CCT AAG CTC CTG ATC      144
998  Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
999    35              40              45
1000
1001 TAT GCT GCA TCC AGT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGC GGC      192
1002 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
1003    50              55              60
1004
1005 AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAA CCT      240
1006 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1007    65              70              75              80
1008
1009 GAA GAT TTT GCA ACT TAT TAC TGT CTA CAG GGT TAT GGT ACC CCG TAC      288
1010 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Gly Tyr Gly Thr Pro Tyr
1011    85              90              95
1012
1013 AGT TTT GGC CAG GGG ACC AAA GTG GAG ATC AAA CGA      324
1014 Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
1015    100              105
1016
1017
1018 (2) INFORMATION FOR SEQ ID NO:24:
1019
1020 (i) SEQUENCE CHARACTERISTICS:
1021 (A) LENGTH: 108 amino acids
1022 (B) TYPE: amino acid
1023 (D) TOPOLOGY: linear
1024
1025 (ii) MOLECULE TYPE: protein
1026
1027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
1028
1029 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1030    1              5              10              15
1031
1032 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
1033    20              25              30
1034
1035 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
1036    35              40              45
1037
1038 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
1039    50              55              60
1040

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## Patent Application US/07/952,640

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1041 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1042 65 70 75 80
1043
1044 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Gly Tyr Gly Thr Pro Tyr
1045 85 90 95
1046
1047 Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
1048 100 105
1049
1050 (2) INFORMATION FOR SEQ ID NO:25:
1051
1052 (i) SEQUENCE CHARACTERISTICS:
1053 (A) LENGTH: 324 base pairs
1054 (B) TYPE: nucleic acid
1055 (C) STRANDEDNESS: both
1056 (D) TOPOLOGY: linear
1057
1058 (ii) MOLECULE TYPE: cDNA
1059
1060 (iii) HYPOTHETICAL: NO
1061
1062 (iv) ANTI-SENSE: NO
1063
1064
1065 (ix) FEATURE:
1066 (A) NAME/KEY: CDS
1067 (B) LOCATION: 1..324
1068
1069
1070 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
1071
1072 GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA 48
1073 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1074 1 5 10 15
1075
1076 GAC ACA GTC ACC ATC ACT TGT CGG GCA AGT CAG GAC ATT AGC AAT AAT 96
1077 Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Asn
1078 20 25 30
1079
1080 TTA GTC TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC 144
1081 Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
1082 35 40 45
1083
1084 TAT GCT GCA TCC AGA TTG CAA GAT GGG GTC CCA TCA AGG TTC AGC GGC 192
1085 Tyr Ala Ala Ser Arg Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly
1086 50 55 60
1087
1088 AGT GGG TCT GGG ACC GAT TTC ACC CTC ACA ATT AAT CCT GTG GAA GCT 240
1089 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala
1090 65 70 75 80
1091
1092 GAC GAT GCT GCG GAT TAC TAC TGT CTA CAG ACT AAG AGT TCT CCT CGG 288

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## Patent Application US/07/952,640

1093 Asp Asp Ala Ala Asp Tyr Tyr Cys Leu Gln Thr Lys Ser Ser Pro Arg  
1094 85 90 95  
1095  
1096 ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGA  
1097 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg  
1098 100 105  
1099  
1100

324

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

1112 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1113 1 5 10 15  
1114  
1115 Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Asn  
1116 20 25 30  
1117  
1118 Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
1119 35 40 45  
1120  
1121 Tyr Ala Ala Ser Arg Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly  
1122 50 55 60  
1123  
1124 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala  
1125 65 70 75 80  
1126  
1127 Asp Asp Ala Ala Asp Tyr Tyr Cys Leu Gln Thr Lys Ser Ser Pro Arg  
1128 85 90 95  
1129  
1130 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg  
1131 100 105  
1132

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

## Patent Application US/07/952,640

1145 (A) NAME/KEY: CDS  
1146 (B) LOCATION: 1..324  
1147  
1148 (ix) FEATURE:  
1149 (A) NAME/KEY: mat\_peptide  
1150 (B) LOCATION: 31..324  
1151  
1152  
1153 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:  
1154  
1155 GACATTCAGC TGACCCAGTC TCCANNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 60  
1156  
1157 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 120  
1158  
1159 NNNNNNNNNN NNCAGCCCTT GATTATGAG GTTTCACACC GGGCCTCTGG AGTCCCAGAC 180  
1160  
1161 AGGTTCAGTG GCAGTGGGTC GGACACTGAT TTCACACTCA AAATCAGCAG AGTGGAGGCT 240  
1162  
1163 GAGGATGTTG GGGTTTATTA CTGCATGCAA TATACACACA TTCCATTAC TTTCGGCCCC 300  
1164  
1165 GGGACCAAAC TGGATATCAA ACGA 324  
1166  
1167 (2) INFORMATION FOR SEQ ID NO:28:  
1168  
1169 (i) SEQUENCE CHARACTERISTICS:  
1170 (A) LENGTH: 108 amino acids  
1171 (B) TYPE: amino acid  
1172 (D) TOPOLOGY: linear  
1173  
1174 (ii) MOLECULE TYPE: protein  
1175  
1176  
1177  
1178 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:  
1179  
1180 Aep Ile Gln Leu Thr Gln Ser Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1181 1 5 10 15  
1182  
1183 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1184 20 25 30  
1185  
1186 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Pro Leu Ile  
1187 35 40 45  
1188  
1189 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Aep Arg Phe Ser Gly  
1190 50 55 60  
1191  
1192 Ser Gly Ser Aep Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala  
1193 65 70 75 80  
1194  
1195 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe  
1196 85 90 95

## Patent Application US/07/952,640

1197  
1198 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg  
1199 100 105  
1200  
1201  
1202  
1203  
1204 (2) INFORMATION FOR SEQ ID NO:29:  
1205  
1206 (i) SEQUENCE CHARACTERISTICS:  
1207 (A) LENGTH: 324 bases  
1208 (B) TYPE: nucleic acid  
1209 (C) STRANDEDNESS: both  
1210 (D) TOPOLOGY: linear  
1211  
1212 (ii) MOLECULE TYPE: cDNA  
1213  
1214 (iii) HYPOTHETICAL: NO  
1215  
1216 (iv) ANTI-SENSE: NO  
1217  
1218  
1219 (ix) FEATURE:  
1220 (A) NAME/KEY: CDS  
1221 (B) LOCATION: 1..324  
1222  
1223  
1224 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:  
1225  
1226 GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA 48  
1227 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1228 1 5 10 15  
1229  
1230 GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AAT TAT 96  
1231 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr  
1232 20 25 30  
1233  
1234 TTA AAT TGG TAT CAA CAG AAA CCA GGG AAA GCC CCT CAG CCC TTG ATT 144  
1235 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile  
1236 35 40 45  
1237  
1238 TAT GAG GTT TCC AAC CGG GCC TCT GGA GTC CCA GAC AGG TTC AGT GGC 192  
1239 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly  
1240 50 55 60  
1241  
1242 AGT GGG TCG GAC ACT GAT TTC ACA CTC AAA ATC AGC AGA GTG GAG GCT 240  
1243 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala  
1244 65 70 75 80  
1245  
1246 GAG GAT GTT GGG GTT TAT TAC TGC ATG CAA TAT ACA CAC ATT CCA TTC 288  
1247 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe  
1248 85 90 95



## Patent Application US/07/952,640

1249  
1250 ACT TTC GGC CCC GGG ACC AAA CTG GAT ATC AAA CGA 324  
1251 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg  
1252 100 105  
1253  
1254  
1255 (2) INFORMATION FOR SEQ ID NO:30:  
1256  
1257 (i) SEQUENCE CHARACTERISTICS:  
1258 (A) LENGTH: 108 amino acids  
1259 (B) TYPE: amino acid  
1260 (D) TOPOLOGY: linear  
1261  
1262 (ii) MOLECULE TYPE: protein  
1263  
1264 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:  
1265  
1266 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1267 1 5 10 15  
1268  
1269 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr  
1270 20 25 30  
1271  
1272 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile  
1273 35 40 45  
1274  
1275 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly  
1276 50 55 60  
1277  
1278 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala  
1279 65 70 75 80  
1280  
1281 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe  
1282 85 90 95  
1283  
1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg  
1285 100 105  
1286  
1287 (2) INFORMATION FOR SEQ ID NO:31  
1288  
1289 (i) SEQUENCE CHARACTERISTICS:  
1290 (A) LENGTH: 324 base pairs  
1291 (B) TYPE: nucleic acid  
1292 (C) STRANDEDNESS: both  
1293 (D) TOPOLOGY: linear  
1294  
1295 (ii) MOLECULE TYPE: cDNA  
1296  
1297 (iii) HYPOTHETICAL: NO  
1298  
1299 (iv) ANTI-SENSE: NO  
1300

## Patent Application US/07/952,640

1301  
1302 (ix) FEATURE:  
1303 (A) NAME/KEY: CDS  
1304 (B) LOCATION: 1..324  
1305  
1306  
1307 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31  
1308  
1309 GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA 48  
1310 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1311 1 5 10 15  
1312  
1313 GAC ACA GTC ACC ATC ACT TGT CGG GCA AGT CAG GGC ATT AGC AAT AAT 96  
1314 Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Aen Aen  
1315 20 25 30  
1316  
1317 TTA GCC TGG TAT CAG CAG AAA CCA GGA AAA GCT CCT AAG CGC CTG ATC 144  
1318 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile  
1319 35 40 45  
1320  
1321 TAT GCT GCA TCC AGT TTG GAA AGT GGG GTC CCA TCA AGG TTC AGT GGC 192  
1322 Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly  
1323 50 55 60  
1324  
1325 AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT 240  
1326 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
1327 65 70 75 80  
1328  
1329 GAA GAT TTT GCA ACT TAT TAC TGT CAA CAG GAT AAC AGT TAT CCT TTC 288  
1330 Glu Aep Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Aen Ser Tyr Pro Phe  
1331 85 90 95  
1332  
1333 ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA 324  
1334 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
1335 100 105  
1336  
1337  
1338 (2) INFORMATION FOR SEQ ID NO:32  
1339  
1340 (i) SEQUENCE CHARACTERISTICS:  
1341 (A) LENGTH: 108 amino acids  
1342 (B) TYPE: amino acid  
1343 (D) TOPOLOGY: linear  
1344  
1345 (ii) MOLECULE TYPE: protein  
1346  
1347 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32  
1348  
1349 Aep Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1350 1 5 10 15  
1351  
1352 Aep Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Aen Aen

## Patent Application US/07/952,640

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1353          20          25          30
1354
1355 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
1356          35          40          45
1357
1358 Tyr Ale Ale Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
1359          50          55          60
1360
1361 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1362          65          70          75          80
1363
1364 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Asn Ser Tyr Pro Phe
1365          85          90          95
1366
1367 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
1368          100         105
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1370 (2) INFORMATION FOR SEQ ID NO:33
1371
1372 (i) SEQUENCE CHARACTERISTICS:
1373 (A) LENGTH: 324 base pairs
1374 (B) TYPE: nucleic acid
1375 (C) STRANDEDNESS: both
1376 (D) TOPOLOGY: linear
1377
1378 (ii) MOLECULE TYPE: cDNA
1379
1380 (iii) HYPOTHETICAL: NO
1381
1382 (iv) ANTI-SENSE: NO
1383
1384
1385 (ix) FEATURE:
1386 (A) NAME/KEY: CDS
1387 (B) LOCATION: 1..324
1388
1389
1390 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33
1391
1392 GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA      48
1393 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1394 1          5          10          15
1395
1396 GAC ACA GTC ACC ATC ACT TGT CGG GCA AGT CAG GGC ATT AGC AAT AAT      96
1397 Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
1398          20          25          30
1399
1400 TTA GCC TGG TAT CAG CAG AAA CCA GGA AAA GCT CCT AAG CGC CTG ATC      144
1401 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
1402          35          40          45
1403
1404 TAT GCT GCA TCC AGT TTG GAA AGT GGG GTC CCA TCA AGG TTC AGT GGC      192

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## Patent Application US/07/952,640

1405 Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly  
1406 50 55 60  
1407  
1408 AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT 240  
1409 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
1410 65 70 75 80  
1411  
1412 GAA GAT TTT GCA ACT TAT TAC TGT CAA CAG GAT AAC AGT TAT CCT TTC 288  
1413 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Asn Ser Tyr Pro Phe  
1414 85 90 95  
1415  
1416 ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA 324  
1417 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
1418 100 105  
1419  
1420  
1421 (2) INFORMATION FOR SEQ ID NO:34  
1422  
1423 (i) SEQUENCE CHARACTERISTICS:  
1424 (A) LENGTH: 108 amino acids  
1425 (B) TYPE: amino acid  
1426 (D) TOPOLOGY: linear  
1427  
1428 (ii) MOLECULE TYPE: protein  
1429  
1430 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34  
1431  
1432 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1433 1 5 10 15  
1434  
1435 Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn  
1436 20 25 30  
1437  
1438 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile  
1439 35 40 45  
1440  
1441 Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly  
1442 50 55 60  
1443  
1444 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
1445 65 70 75 80  
1446  
1447 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Asn Ser Tyr Pro Phe  
1448 85 90 95  
1449  
1450 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
1451 100 105  
1452  
1453 (2) INFORMATION FOR SEQ ID NO:35:  
1454  
1455 (i) SEQUENCE CHARACTERISTICS:  
1456 (A) LENGTH: 342 base pairs

## Patent Application US/07/952,640

1457 (B) TYPE: nucleic acid  
1458 (C) STRANDEDNESS: both  
1459 (D) TOPOLOGY: linsar  
1460

1461 (ii) MOLECULE TYPE: cDNA  
1462  
1463

1464 (ix) FEATURE:

1465 (A) NAME/KEY: CDS  
1466 (B) LOCATION: 1..342  
1467  
1468

1469 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:  
1470

1471	GAC	ATT	GTG	ATG	ACT	CAG	TCT	CCA	ACT	TTC	CTT	GCT	GTG	ACA	GCA	AGT	48
1472	Asp	Ils	Val	Mst	Thr	Gln	Ssr	Pro	Thr	Phs	Lsu	Ala	Val	Thr	Ala	Ssr	
1473	1				5					10						15	
1474																	
1475	AAG	AAG	GTC	ACC	ATT	AGT	TGC	ACT	GCC	TCT	GAG	AGC	CTT	TAT	TCA	AGC	96
1476	Lys	Lys	Val	Thr	Ils	Ssr	Cys	Thr	Ala	Ser	Glu	Ssr	Leu	Tyr	Ser	Ssr	
1477				20				25						30			
1478																	
1479	AAA	CAC	AAG	GTG	CAC	TAC	TTG	GCT	TGG	TAC	CAG	AAG	AAA	CCA	GAG	CAA	144
1480	Lys	His	Lys	Val	His	Tyr	Leu	Ala	Trp	Tyr	Gln	Lys	Lys	Pro	Glu	Gln	
1481			35					40						45			
1482																	
1483	TCT	CCT	AAA	CTG	CTG	ATA	TAC	GGG	GCA	TCC	AAC	CGA	TAC	ATT	GGG	GTC	192
1484	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Gly	Ala	Ssr	Asn	Arg	Tyr	Ile	Gly	Val	
1485			50				55					60					
1486																	
1487	CCT	GAT	CGC	TTC	ACA	GGC	AGT	GGA	TCT	GGG	ACA	GAT	TTC	ACT	CTG	ACC	240
1488	Pro	Asp	Arg	Phs	Thr	Gly	Ssr	Gly	Ssr	Gly	Thr	Asp	Phe	Thr	Lsu	Thr	
1489	65					70				75					80		
1490																	
1491	ATC	AGC	AGT	GTA	CAG	GTT	GAA	GAC	CTC	ACA	CAT	TAT	TAC	TGT	GCA	CAG	288
1492	Ils	Ser	Ser	Val	Gln	Val	Glu	Asp	Lsu	Thr	His	Tyr	Tyr	Cys	Ala	Gln	
1493				85						90					95		
1494																	
1495	TTT	TAC	AGC	TAT	CCT	CTC	ACG	TTC	GGT	GCT	GGG	ACC	AAG	CTG	GAG	CTG	336
1496	Phs	Tyr	Ser	Tyr	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Lsu	Glu	Lsu	
1497				100					105					110			
1498																	
1499	AAA	CGG															342
1500	Lys	Arg															
1501																	
1502																	
1503																	

1504 (2) INFORMATION FOR SEQ ID NO:36:

1505

1506 (i) SEQUENCE CHARACTERISTICS:

1507 (A) LENGTH: 114 amino acids

1508 (B) TYPE: amino acid

## Patent Application US/07/952,640

1509 (D) TOPOLOGY: linear  
1510  
1511 (ii) MOLECULE TYPE: protein  
1512  
1513 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:  
1514  
1515 Asp Ile Val Met Thr Gln Ser Pro Thr Phe Leu Ala Val Thr Ala Ser  
1516 1 5 10 15  
1517  
1518 Lys Lys Val Thr Ile Ser Cys Thr Ala Ser Glu Ser Leu Tyr Ser Ser  
1519 20 25 30  
1520  
1521 Lys His Lys Val His Tyr Leu Ala Trp Tyr Gln Lys Lys Pro Glu Gln  
1522 35 40 45  
1523  
1524 Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Ile Gly Val  
1525 50 55 60  
1526  
1527 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
1528 65 70 75 80  
1529  
1530 Ile Ser Ser Val Gln Val Glu Asp Leu Thr His Tyr Tyr Cys Ala Gln  
1531 85 90 95  
1532  
1533 Phe Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu  
1534 100 105 110  
1535  
1536 Lys Arg  
1537  
1538  
1539 (2) INFORMATION FOR SEQ ID NO:37:  
1540  
1541 (i) SEQUENCE CHARACTERISTICS:  
1542 (A) LENGTH: 327 base pairs  
1543 (B) TYPE: nucleic acid  
1544 (C) STRANDEDNESS: both  
1545 (D) TOPOLOGY: linear  
1546  
1547 (ii) MOLECULE TYPE: cDNA  
1548  
1549 (iii) HYPOTHETICAL: NO  
1550  
1551 (iv) ANTI-SENSE: NO  
1552  
1553  
1554 (ix) FEATURE:  
1555 (A) NAME/KEY: CDS  
1556 (B) LOCATION: 1..327  
1557  
1558  
1559 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37  
1560

## Patent Application US/07/952,640

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1561 GCC CTC GTG ATG ACC CAG ACT CCA GCC TCC GTG TCT GCA GCT GTG GGA      48
1562 Ala Leu Val Met Thr Gln Thr Pro Ala Ser Val Ser Ala Ala Val Gly
1563   1                      5                      10                      15
1564
1565 GGC ACA GTC ACC ATC AAG TGC CAG GCC AGT GAG AAC ATT TAC AGC TCT      96
1566 Gly Thr Val Thr Ile Lys Cys Gln Ala Ser Glu Aen Ile Tyr Ser Ser
1567           20                      25                      30
1568
1569 TTA GCC TGG TAT CAG CAG AAA CCA GGG CAG CCT CCC AAG CTC CTG ATC      144
1570 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
1571           35                      40                      45
1572
1573 TAT GGT GCA TCC ACT CTG GCA TCT GGG GTC CCA TCG CGG TTC AAA GGC      192
1574 Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys Gly
1575           50                      55                      60
1576
1577 AGT AGA TCT GGG ACA GAG TAC ACT CTC ACC ATC AGC GGC GTG CAG CGT      240
1578 Ser Arg Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Gly Val Gln Arg
1579   65                      70                      75                      80
1580
1581 GAG GAT GCT GCC ACC TAC TAC TGT CTA GGC AGT GAT AGT AGT AGC GAT      288
1582 Glu Aep Ala Ala Thr Tyr Tyr Cys Leu Gly Ser Aep Ser Ser Ser Asp
1583           85                      90                      95
1584
1585 ACT GCT TTC GGC GGA GGG ACC GAG CTG GAG ATC CTA TGT      327
1586 Thr Ala Phe Gly Gly Gly Thr Glu Leu Glu Ile Leu Cys
1587           100                      105
1588
1589
1590 (2) INFORMATION FOR SEQ ID NO:38:
1591
1592 (i) SEQUENCE CHARACTERISTICS:
1593 (A) LENGTH: 109 amino acids
1594 (B) TYPE: amino acid
1595 (D) TOPOLOGY: linear
1596
1597 (ii) MOLECULE TYPE: protein
1598
1599 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
1600
1601 Ala Leu Val Met Thr Gln Thr Pro Ala Ser Val Ser Ala Ala Val Gly
1602   1                      5                      10                      15
1603
1604 Gly Thr Val Thr Ile Lys Cys Gln Ala Ser Glu Asn Ile Tyr Ser Ser
1605           20                      25                      30
1606
1607 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
1608           35                      40                      45
1609
1610 Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys Gly
1611           50                      55                      60
1612
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## Patent Application US/07/952,640

1613 Ser Arg Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Gly Val Gln Arg  
1614 65 70 75 80  
1615  
1616 Glu Asp Ala Ala Thr Tyr Tyr Cys Leu Gly Ser Asp Ser Ser Ser Asp  
1617 85 90 95  
1618  
1619 Thr Ala Phe Gly Gly Gly Thr Glu Leu Glu Ile Leu Cys  
1620 100 105  
1621

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..321

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

1643  
1644 ACT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG CAG 48  
1645 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
1646 1 5 10 15  
1647  
1648 TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT 96  
1649 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
1650 20 25 30  
1651  
1652 CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG 144  
1653 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
1654 35 40 45  
1655  
1656 GGT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC 192  
1657 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
1658 50 55 60  
1659  
1660 TAC AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA 240  
1661 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
1662 65 70 75 80  
1663  
1664 CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC 288



## Patent Application US/07/952,640

1665 Hie Lye Val Tyr Ala Cye Glu Val Thr Hie Gln Gly Leu Ser Ser Pro  
1666 85 90 95  
1667  
1668 GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT TA  
1669 Val Thr Lye Ser Phe Aen Arg Gly Glu Cys  
1670 100 105  
1671  
1672

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

1684 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Aep Glu Gln  
1685 1 5 10 15  
1686  
1687 Leu Lye Ser Gly Thr Ala Ser Val Val Cys Leu Leu Aen Asn Phe Tyr  
1688 20 25 30  
1689  
1690 Pro Arg Glu Ala Lye Val Gln Trp Lye Val Aep Aen Ala Leu Gln Ser  
1691 35 40 45  
1692  
1693 Gly Aen Ser Gln Glu Ser Val Thr Glu Gln Aep Ser Lye Aep Ser Thr  
1694 50 55 60  
1695  
1696 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lye Ala Aep Tyr Glu Lye  
1697 65 70 75 80  
1698  
1699 Hie Lys Val Tyr Ala Cye Glu Val Thr Hie Gln Gly Leu Ser Ser Pro  
1700 85 90 95  
1701  
1702 Val Thr Lye Ser Phe Aen Arg Gly Glu Cye  
1703 100 105  
1704  
1705

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: YES

321

are listed  
on this line

320 listed

## Patent Application US/07/952,640

1717  
1718 (iv) ANTI-SENSE: NO  
1719  
1720  
1721 (ix) FEATURE:  
1722 (A) NAME/KEY: CDS  
1723 (B) LOCATION: 1..321  
1724  
1725  
1726 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:  
1727  
1728 GCT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAG GAT CAG 48  
1729 Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Glu Asp Gln  
1730 1 5 10 15  
1731  
1732 GTG AAA TCT GGA ACT GTC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT 96  
1733 Val Lys Ser Gly Thr Val Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
1734 20 25 30  
1735  
1736 CCC AGA GAG GCC AGC GTA AAG TGG AAG GTG GAT GGT GCC CTC AAA ACG 144  
1737 Pro Arg Glu Ala Ser Val Lys Trp Lys Val Asp Gly Ala Leu Lys Thr  
1738 35 40 45  
1739  
1740 GAT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC AAG GAC AAC ACC 192  
1741 Asp Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Asn Thr  
1742 50 55 60  
1743  
1744 TAC AGC CTG AGC AGC ACC CTG ACG CTG AGC AGC ACA GAC TAC CAG AGT 240  
1745 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Ser Thr Asp Tyr Gln Ser  
1746 65 70 75 80  
1747  
1748 CAC AAT GTC TAT GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC 288  
1749 His Asn Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro  
1750 85 90 95  
1751  
1752 GTC ACC AAG AGC TTC AAC AGG GGA GAG TGT TA  
1753 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
1754 100 105  
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1756  
1757 (2) INFORMATION FOR SEQ ID NO:42:  
1758  
1759 (i) SEQUENCE CHARACTERISTICS:  
1760 (A) LENGTH: 106 amino acids  
1761 (B) TYPE: amino acid  
1762 (D) TOPOLOGY: linear  
1763  
1764 (ii) MOLECULE TYPE: protein  
1765  
1766 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:  
1767  
1768 Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Glu Asp Gln

321  
320

## Patent Application US/07/952,640

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1769      1              5              10              15
1770
1771 Val Lys Ser Gly Thr Val Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
1772      20              25              30
1773
1774 Pro Arg Glu Ala Ser Val Lys Trp Lys Val Asp Gly Ala Leu Lys Thr
1775      35              40              45
1776
1777 Asp Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Asn Thr
1778      50              55              60
1779
1780 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Ser Thr Asp Tyr Gln Ser
1781      65              70              75              80
1782
1783 His Asn Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
1784      85              90              95
1785
1786 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1787      100             105
1788
1789
1790 (2) INFORMATION FOR SEQ ID NO:43:
1791
1792 (i) SEQUENCE CHARACTERISTICS:
1793 (A) LENGTH: 321 base pairs
1794 (B) TYPE: nucleic acid
1795 (C) STRANDEDNESS: both
1796 (D) TOPOLOGY: linear
1797
1798 (ii) MOLECULE TYPE: cDNA
1799
1800 (iii) HYPOTHETICAL: NO
1801
1802 (iv) ANTI-SENSE: NO
1803
1804
1805 (ix) FEATURE:
1806 (A) NAME/KEY: CDS
1807 (B) LOCATION: 1..321
1808
1809
1810 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:
1811
1812 GAT CCA ATT GCG CCT ACT GTC CTC CTC TTC CCA CCA TCT GCT GAT CAG      48
1813 Asp Pro Ile Ala Pro Thr Val Leu Leu Phe Pro Pro Ser Ala Asp Gln
1814      1              5              10              15
1815
1816 CTG ACA ACT GAA ACA GTC ACC ATC GTG TGC GTG GCA AAT AAA TTC CGT      96
1817 Leu Thr Thr Glu Thr Val Thr Ile Val Cys Val Ala Asn Lys Phe Arg
1818      20              25              30
1819
1820 CCC AAT GAC ATC ACC GTC ACC TGG AAG GTG GAT GAC GAA ATC CAA CAG      144

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320 listed

## Patent Application US/07/952,640

1821 Pro Asn Asp Ile Thr Val Thr Trp Lys Val Asp Asp Glu Ile Gln Gln  
1822 35 40 45  
1823  
1824 AGC GGC TTC GAG AAC AGT ACA ACA CCG CAG AGC CCC GAG GAC TGT ACC 192  
1825 Ser Gly Phe Glu Asn Ser Thr Thr Pro Gln Ser Pro Glu Asp Cys Thr  
1826 50 55 60  
1827  
1828 TAC AAC CTC AGC AGC ACT CTG TCA CTG ACC AAA GCA CAG TAC AAC AGC 240  
1829 Tyr Asn Leu Ser Ser Thr Leu Ser Leu Thr Lys Ala Gln Tyr Asn Ser  
1830 65 70 75 80  
1831  
1832 CAC AGC GTG TAC ACC TGC GAG GTG GTC CAT CAC AAC TCG GGC TCA GCG 288  
1833 His Ser Val Tyr Thr Cys Glu Val Val His His Asn Ser Gly Ser Ala  
1834 85 90 95  
1835  
1836 ATC GTC CAG AGC TTC AAT AGG GGT GAC TGT TA  
1837 Ile Val Gln Ser Phe Asn Arg Gly Asp Cys  
1838 100 105  
1839  
1840  
1841 (2) INFORMATION FOR SEQ ID NO:44:  
1842  
1843 (i) SEQUENCE CHARACTERISTICS:  
1844 (A) LENGTH: 106 amino acids  
1845 (B) TYPE: amino acid  
1846 (D) TOPOLOGY: linear  
1847  
1848 (ii) MOLECULE TYPE: protein  
1849  
1850 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:  
1851  
1852 Asp Pro Ile Ala Pro Thr Val Leu Leu Phe Pro Pro Ser Ala Asp Gln  
1853 1 5 10 15  
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1855 Leu Thr Thr Glu Thr Val Thr Ile Val Cys Val Ala Asn Lys Phe Arg  
1856 20 25 30  
1857  
1858 Pro Asn Asp Ile Thr Val Thr Trp Lys Val Asp Asp Glu Ile Gln Gln  
1859 35 40 45  
1860  
1861 Ser Gly Phe Glu Asn Ser Thr Thr Pro Gln Ser Pro Glu Asp Cys Thr  
1862 50 55 60  
1863  
1864 Tyr Asn Leu Ser Ser Thr Leu Ser Leu Thr Lys Ala Gln Tyr Asn Ser  
1865 65 70 75 80  
1866  
1867 His Ser Val Tyr Thr Cys Glu Val Val His His Asn Ser Gly Ser Ala  
1868 85 90 95  
1869  
1870 Ile Val Gln Ser Phe Asn Arg Gly Asp Cys  
1871 100 105  
1872

321

320

## Patent Application US/07/952,640

1873  
1874  
1875 (2) INFORMATION FOR SEQ ID NO:45:  
1876  
1877 (i) SEQUENCE CHARACTERISTICS:  
1878 (A) LENGTH: 321 base pairs  
1879 (B) TYPE: nucleic acid  
1880 (C) STRANDEDNESS: both  
1881 (D) TOPOLOGY: linear  
1882  
1883 (ii) MOLECULE TYPE: cDNA  
1884  
1885 (iii) HYPOTHETICAL: NO  
1886  
1887 (iv) ANTI-SENSE: NO  
1888  
1889  
1890 (ix) FEATURE:  
1891 (A) NAME/KEY: CDS  
1892 (B) LOCATION: 1..321  
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1895 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:  
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1898 Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln  
1899 1 5 10 15  
1900  
1901 TTA ACA TCT GGA GGT GCC TCA GTC GTG TGC TTC TTG AAC AAC TTC TAC 96  
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1903 20 25 30  
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1906 Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln  
1907 35 40 45  
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1910 Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr  
1911 50 55 60  
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1913 TAC AGC ATG AGC AGC ACC CTC ACG TTG ACC AAG GAC GAG TAT GAA CGA 240  
1914 Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg  
1915 65 70 75 80  
1916  
1917 CAT AAC AGC TAT ACC TGT GAG GCC ACT CAC AAG ACA TCA ACT TCA CCC 288  
1918 His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro  
1919 85 90 95  
1920  
1921 ATT GTC AAG AGC TTC AAC AGG AAT GAG TGT TA 321  
1922 Ile Val Lys Ser Phe Asn Arg Asn Glu Cys  
1923 100 105  
1924

← same error

## Patent Application US/07/952,640

1925

1926 (2) INFORMATION FOR SEQ ID NO:46:

1927

1928 (i) SEQUENCE CHARACTERISTICS:

1929 (A) LENGTH: 106 amino acids

1930 (B) TYPE: amino acid

1931 (D) TOPOLOGY: linear

1932

1933 (ii) MOLECULE TYPE: protein

1934

1935 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

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1937	Ala	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ile	Phe	Pro	Pro	Ser	Ser	Glu	Gln
1938	1				5					10					15	

1939

1940	Leu	Thr	Ser	Gly	Gly	Ala	Ser	Val	Val	Cys	Phe	Leu	Asn	Asn	Phe	Tyr
1941				20					25					30		

1942

1943	Pro	Lys	Asp	Ile	Asn	Val	Lys	Trp	Lys	Ile	Asp	Gly	Ser	Glu	Arg	Gln
1944			35					40					45			

1945

1946	Asn	Gly	Val	Leu	Asn	Ser	Trp	Thr	Asp	Gln	Asp	Ser	Lys	Asp	Ser	Thr
1947		50						55				60				

1948

1949	Tyr	Ser	Met	Ser	Ser	Thr	Leu	Thr	Leu	Thr	Lys	Asp	Glu	Tyr	Glu	Arg
1950	65					70					75				80	

1951

1952	His	Asn	Ser	Tyr	Thr	Cys	Glu	Ala	Thr	His	Lys	Thr	Ser	Thr	Ser	Pro
1953					85					90					95	

1954

1955	Ile	Val	Lys	Ser	Phe	Asn	Arg	Asn	Glu	Cys						
1956				100					105							

1957

PAGE: 1

SEQUENCE VERIFICATION REPORT  
PATENT APPLICATION US/07/952,640

DATE: 06/27/93  
TIME: 13:10:31  
S5963

LINE ERROR

ORIGINAL TEXT

28 Wrong application Serial Number  
572 Wrong Amino Acid Designator  
572 Wrong Amino Acid Designator  
572 Wrong Amino Acid Designator  
572 Wrong Amino Acid Designator  
572 Wrong Amino Acid Designator  
572 Wrong Amino Acid Designator  
592 Wrong Sequence Number  
623  
1642 Entered and Calc. Seq. Length differ  
1726 Entered and Calc. Seq. Length differ  
1810 Entered and Calc. Seq. Length differ  
1895 Entered and Calc. Seq. Length differ  
11 Number of Sequences Doesn't Equal Actual

(A) APPLICATION NUMBER: US 07/952640  
210 215 (2) INFORMA  
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:  
Sequence 13 missing  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:  
(iii) NUMBER OF SEQUENCES: 46

PAGE: 1

SEQUENCE MISSING ITEM REPORT  
PATENT APPLICATION US/07/952,640

DATE: 06/27/93  
TIME: 13:10:31  
S5963

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA  
APPLICATION NUMBER  
FILING DATE



PAGE: 1

SEQUENCE CORRECTION REPORT  
PATENT APPLICATION US/07/952,640

DATE: 06/27/93  
TIME: 13:10:31  
S5963

LINE ORIGINAL TEXT

CORRECTED TEXT

1287 (2) INFORMATION FOR SEQ ID NO:31  
1307 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31  
1338 (2) INFORMATION FOR SEQ ID NO:32  
1347 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32  
1370 (2) INFORMATION FOR SEQ ID NO:33  
1390 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33  
1421 (2) INFORMATION FOR SEQ ID NO:34  
1430 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34  
1559 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

(2) INFORMATION FOR SEQ ID NO:31:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:  
(2) INFORMATION FOR SEQ ID NO:32:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:  
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37: